

1 |-----A-----|-----
TCAAATTTT CTCCAGTTCT AAATATCCGG AACCTCTTG GGATGCCATT

51 -----B-----|-----C-----|---D---
GCCCATCTAT CTGTAATTTA TTGACGAAAT AGACGAAAAG GAAGGTGGCT

101 -|-----E-----|-----F-----|
CCTATAAAGC ACATCATTGC GATAACAGAA AGGCCATTGT TGAAGATACC

151 |-----G-----|-----H-----|-----
TCTGCTGACA TTGGTCCCA AGTGGAAGCA CCACCCCATG AGGAGCACCG

201 --F--|-----G-----|-----I-----
TGGAGTAAGA AGACGTTCTGA GCCACGTCGA AAAAGCAAGT GTGTTGATGT

251 ----|-----J-----|-----K-----|-----L-----
AGTATCTCCA TTGACGTAAG GGATGAACA CAATCCAACAT ATCCATCGCA

301 -----|-----M-----|-----L-----|---N-
AGACCATTGC TCTATATAAG AAAGTTAATA TCATTTCGAG TGGCCACGCT

351 |
G [SEQ ID NO:1]

FIGURE 1

1 TCAAATTTTT CTCCAGTTCT AAATATCCGG AAACCTCTTG GGATGCCATT
51 GCCCATCTAT CTGTAATTTA TTGACGAAAT AGACGAAAAG GAAGGTGGCT
101 CCTATAAAGC ACATCATTGC GATAACAGAA AGGCCATTGT TGAAGATACC
151 TCTGCTGACA TTGGTCCCCA AGTGGAAGCA CCACCCCATG AGGAGCACCG
201 TGGAGTAAGA AGACGTTCGA GCCACGTCGA AAAAGCAAGT GTGTTGATGT
251 AGTATCTCCA TTGACGTAAG GGATGACGCA CAATCCAACT ATCCATCGCA
301 AGACCATTGC TCTATATAAG AAAGTTAATA TCATTTCGAG TGGCCACGCT
351 G [SEQ ID NO:2]

FIGURE 2

1 TCAAATTTTT CTCCAGTTCT AAATATCCGG AACCTCTTG GGATGCCATT
| | | | | | | | | | | | | | | | | | | | | |
TGAGACTTTT CAACAAAGGG TAATATCGGG AACCTCCTC GGATTCCATT

51 GCCCATCTAT CTGT-AATTT ATTGACGAAA TAGACGAAAA GGAAGGTGGC
| | | | | | | | | | | | | | | | | | | | | |
GCCCAGCTAT CTGTCACTTC ATCAAAGGA CAGTAGAAAA GGAAGGTGGC

101 TCCTATAAAG CACATCATTG CGATAACAGA AAGGCCATTG TTGAAGATAC
| | | | | | | | | | | | | | | | | | | | | |
ACCTACAAAT GCCATCATTG CGATAAAGGA AAGGCTATCG TTCAAGATGC

151 CTCTGCTGAC ATTGGTCCCC AAGTGAAGC ACCACCCCAT GAGGAGCACC
| | | | | | | | | | | | | | | | | | | | | |
CTCTGCCGAC AGTGGTCCCCA AAGATGGACC CCCA-CCCAC GAGGAGCATC

201 GTGGAGTAAG AAGACGTTCG AGCCACGTCG AAAAAGCAAG TGTGTTGATG
| | | | | | | | | | | | | | | | | | | | | |
GTGGAAAAAG AAGACGTTC C AACCACGTCT TCAAAGCAAG TGGATTGATG

251 TAGTATCTCC ATTGACGTAA GGGATGACGC ACAATCCAAC TATCCATCGC
| | | | | | | | | | | | | | | | | | | | | |
TCATATCTCC ACTGACGTAA GGGATGACGC ACAATCCCAC TATCCTTCGC

301 AAGACCATTG CTCTATATAA GAAAGTTAAT ATCATTTCTGA GTGGCCACGC
| | | | | | | | | | | | | | | | | | | | | |
AAGACCCTTC CTCTATATAA GGAAGTTCAT TTCATTTGGA GAGGACACGC

351 TG [SEQ ID NO:2]
| |
TG [SEQ ID NO:3]

FIGURE 3

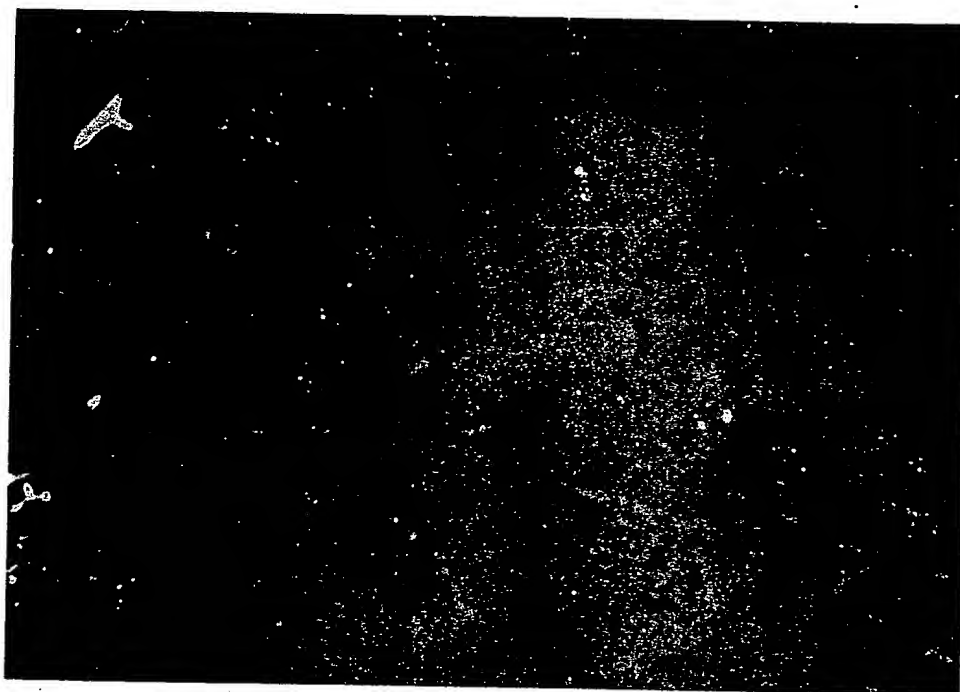


FIG. 4A

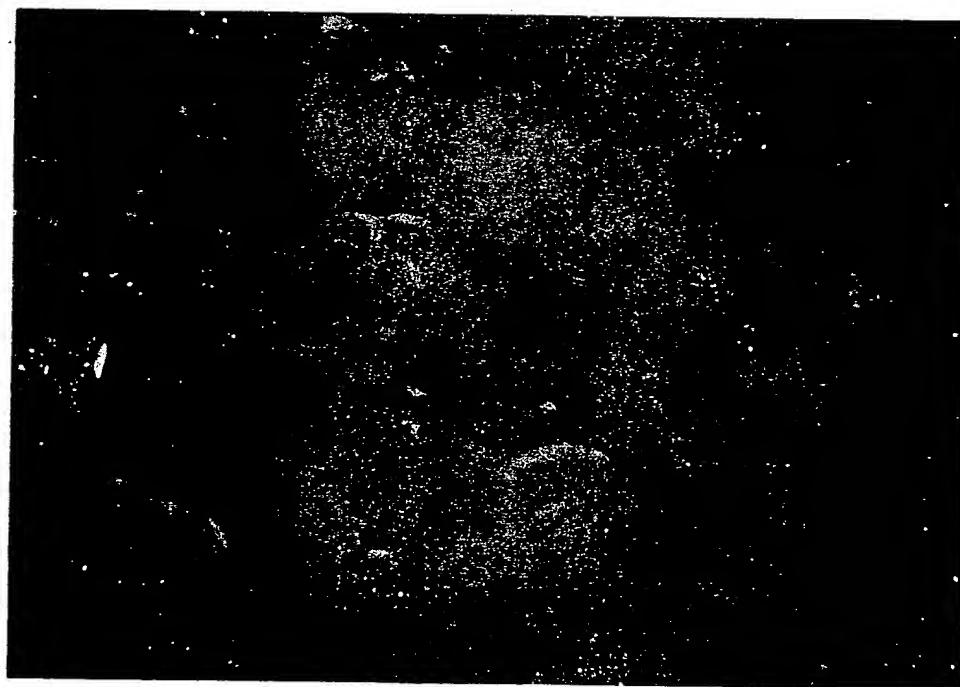


FIG. 4B